

SEQUENCE LISTING

<110> Delagrave, Simon

<120> BIOTHERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS

<130> BTS 0002-500

<160> 28

<170> PatentIn version 3.3

<210> 1

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> hCASK-PDZopt

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attgaatcat tgtattgttg cccgtattat gcatgggtgg atgattcatc gtcaagggtac 180

tttgcattgt ggtgatgaaa ttcgtgaaat taatgggtatt tctgttgcca atcaaaccgt 240

tgaacaattg caaaaaatgt tgcgtgaaat gcgtgggttct attaccttta aaattgttcc 300

atcttatcgt acccaatctt cttctggaat tcatgcggcc gctgggtgctc cagt 354

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1 5 10 15Lys Asn Thr Asp Glu Pro Met Gly Ile Thr Leu Lys Met Asn Glu Leu
20 25 30Asn His Cys Ile Val Ala Arg Ile Met His Gly Gly Met Ile His Arg
35 40 45Gln Gly Thr Leu His Val Gly Asp Glu Ile Arg Glu Ile Asn Gly Ile
50 55 60Ser Val Ala Asn Gln Thr Val Glu Gln Leu Gln Lys Met Leu Arg Glu
65 70 75 80

Met Arg Gly Ser Ile Thr Phe Lys Ile Val Pro Ser Tyr Arg Thr Gln
85 90 95

Ser Ser Ser

<210> 3
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<212> PRT
<213> Artificial Sequence

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<223> hCASK-PDZ-GST fusion

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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Gly Met Asp Met Glu Asn Val
 225 230 235 240
 Thr Arg Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met
 245 250 255
 Gly Ile Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg
 260 265 270
 Ile Met His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly
 275 280 285
 Asp Glu Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val
 290 295 300
 Glu Gln Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe
 305 310 315 320
 Lys Ile Val Pro Ser Tyr Arg Thr Gln Ser Ser Ser Gly Ile His Arg
 325 330 335

Asp

<210> 4
 <211> 590
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 <213> Artificial Sequence

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 <223> hCASK-PDZ-alkaline phosphatase fusion

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 Phe Cys Leu Pro Val Phe Ala Gly Met Asp Met Glu Asn Val Thr Arg
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 Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile
 35 40 45

Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met
 50 55 60
 His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu
 65 70 75 80
 Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln
 85 90 95
 Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile
 100 105 110
 Val Pro Ser Tyr Arg Thr Gln Ser Ser Ser Arg Thr Pro Glu Met Pro
 115 120 125
 Leu Gln Gly Thr Ala Val Asp Gly Gly Gly Gly Ser Met His Ala Ser
 130 135 140
 Leu Glu Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro
 145 150 155 160
 Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp
 165 170 175
 Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp
 180 185 190
 Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly
 195 200 205
 Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln
 210 215 220
 Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val
 225 230 235 240
 Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr
 245 250 255
 Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys Asp His Pro Thr
 260 265 270
 Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser
 275 280 285
 Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu Val Ala His Val
 290 295 300

Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro
 305 310 315 320
 Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu
 325 330 335
 Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe
 340 345 350
 Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu
 355 360 365
 Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu
 370 375 380
 Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe
 385 390 395 400
 Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr
 405 410 415
 His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln
 420 425 430
 Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile
 435 440 445
 Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly
 450 455 460
 Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile
 465 470 475 480
 Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe
 485 490 495
 Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr Ala Asp His Ala
 500 505 510
 His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr
 515 520 525
 Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly
 530 535 540
 Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile
 545 550 555 560

Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly Leu Thr Asp Gln
565 570 575

Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly Leu Lys
580 585 590

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<212> PRT
<213> Artificial Sequence

<220>
<223> hCASK-PDZ-fc fusion protein

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Met Arg Ala Pro Ala Gln Ile Phe Gly Phe Leu Leu Leu Leu Phe Pro
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Gly Thr Arg Cys Gly Met Asp Met Glu Asn Val Thr Arg Val Arg Leu
20 25 30

Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile Thr Leu Lys
35 40 45

Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met His Gly Gly
50 55 60

Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu Ile Arg Glu
65 70 75 80

Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln Leu Gln Lys
85 90 95

Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile Val Pro Ser
100 105 110

Tyr Arg Thr Gln Ser Ser Ser Glu Pro Lys Ser Cys Asp Lys Thr His
115 120 125

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
130 135 140

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
145 150 155 160

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
165 170 175

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
180 185 190

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
195 200 205

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Asp Tyr Lys
210 215 220

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Met Gln Lys Thr Ile
225 230 235 240

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
245 250 255

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
260 265 270

Val Lys Gly Phe Tyr Pro Arg His Ile Ala Val Glu Trp Glu Ser Asn
275 280 285

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
290 295 300

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
305 310 315 320

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
325 330 335

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
340 345 350

<210> 6
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> polyhistidine tagged and secreted hCASK-PDZ

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Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1 5 10 15

Phe Cys Leu Pro Val Phe Ala Gly Met Asp Met Glu Asn Val Thr Arg
20 25 30

Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile
35 40 45

Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met
50 55 60

His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu
65 70 75 80

Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln
85 90 95

Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile
100 105 110

Val Pro Ser Tyr Arg Thr Gln Ser Ser Ser His His His His His His
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<210> 7
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> secreted hCASK-PDZ

<400> 7

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1 5 10 15

Phe Cys Leu Pro Val Phe Ala Gly Met Asp Met Glu Asn Val Thr Arg
20 25 30

Val Arg Leu Val Gln Phe Gln Lys Asn Thr Asp Glu Pro Met Gly Ile
35 40 45

Thr Leu Lys Met Asn Glu Leu Asn His Cys Ile Val Ala Arg Ile Met
50 55 60

His Gly Gly Met Ile His Arg Gln Gly Thr Leu His Val Gly Asp Glu
65 70 75 80

Ile Arg Glu Ile Asn Gly Ile Ser Val Ala Asn Gln Thr Val Glu Gln
85 90 95

Leu Gln Lys Met Leu Arg Glu Met Arg Gly Ser Ile Thr Phe Lys Ile
100 105 110

Val Pro Ser Tyr Arg Thr Gln Ser Ser Ser
115 120

<210> 8
<211> 234

<212> PRT

<213> Artificial Sequence

<220>

<223> NHERF PDZ dimer

<400> 8

Pro Arg Leu Cys Cys Leu Glu Lys Gly Pro Asn Gly Tyr Gly Phe His
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Leu His Gly Glu Lys Gly Lys Leu Gly Gln Tyr Ile Arg Leu Val Glu
 20 25 30

Pro Gly Ser Pro Ala Glu Lys Ala Gly Leu Leu Ala Gly Asp Arg Leu
 35 40 45

Val Glu Val Asn Gly Glu Asn Val Glu Lys Glu Thr His Gln Gln Val
 50 55 60

Val Ser Arg Ile Arg Ala Ala Leu Asn Ala Val Arg Leu Leu Val Val
 65 70 75 80

Asp Pro Glu Thr Asp Glu Gln Leu Gln Lys Leu Gly Val Gln Val Arg
 85 90 95

Glu Glu Leu Leu Arg Ala Gln Glu Ala Pro Gly Gln Ala Glu Pro Pro
 100 105 110

Ala Ala Ala Glu Val Gln Gly Ala Gly Asn Glu Asn Glu Pro Arg Glu
 115 120 125

Ala Asp Lys Ser His Pro Glu Gln Arg Glu Leu Arg Pro Arg Leu Cys
 130 135 140

Thr Met Lys Lys Gly Pro Ser Gly Tyr Gly Phe Asn Leu His Ser Asp
 145 150 155 160

Lys Ser Lys Pro Gly Gln Phe Ile Arg Ser Val Asp Pro Asp Ser Pro
 165 170 175

Ala Glu Ala Ser Gly Leu Arg Ala Gln Asp Arg Ile Val Glu Val Asn
 180 185 190

Gly Val Cys Met Glu Gly Lys Gln His Gly Asp Val Val Ser Ala Ile
 195 200 205

Arg Ala Gly Gly Asp Glu Thr Lys Leu Leu Val Val Asp Arg Glu Thr
 210 215 220

Asp Glu Phe Phe Lys Lys Cys Arg Val Ile
225 230

<210> 9
<211> 546
<212> PRT
<213> Artificial Sequence

<220>
<223> third PDZ domain of human Dlg1
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Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ala
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Ala Gln Pro Ala Ala Val Leu Gly Asp Asp Glu Ile Thr Arg Glu Pro
20 25 30

Arg Lys Val Val Leu His Arg Gly Ser Thr Gly Leu Gly Phe Asn Ile
35 40 45

Val Gly Gly Glu Asp Gly Glu Gly Ile Phe Ile Ser Phe Ile Leu Ala
50 55 60

Gly Gly Pro Ala Asp Leu Ser Gly Glu Leu Arg Lys Gly Asp Arg Ile
65 70 75 80

Ile Ser Val Asn Ser Val Asp Leu Arg Ala Ala Ser His Glu Gln Ala
85 90 95

Ala Ala Ala Leu Lys Asn Ala Gly Gln Ala Val Thr Ile Val Ala Gln
100 105 110

Tyr Arg Pro Glu Glu Tyr Ser Arg Phe Glu Ala Ala Ala Ala Gly Ala
115 120 125

Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala Gln Thr Val
130 135 140

Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser Phe Thr Asn Val
145 150 155 160

Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys
165 170 175

Leu Trp Asn Ala Thr Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln
180 185 190

Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu
195 200 205

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
 210 215 220
 Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr
 225 230 235 240
 Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln
 245 250 255
 Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn
 260 265 270
 Thr Phe Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu
 275 280 285
 Thr Val Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr
 290 295 300
 Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr
 305 310 315 320
 Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu
 325 330 335
 Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln
 340 345 350
 Pro Pro Val Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 355 360 365
 Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
 370 375 380
 Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr
 385 390 395 400
 Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp
 405 410 415
 Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala
 420 425 430
 Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly
 435 440 445
 Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser
 450 455 460

Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn
465 470 475 480

Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro
485 490 495

Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp
500 505 510

Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala
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Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys
530 535 540

Glu Ser
545

<210> 10
<211> 485
<212> DNA
<213> Artificial Sequence

<220>
<223> third PDZ domain of human Dlg1

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cttggtttca acattgtagg aggagaagat ggagaaggaa tttttatttc ctttatctta 180
gccggaggac ctgctgatct aagtggagag ctcagaaaag gagatcgat tatatcggtta 240
aacagtgttg acctcagagc tgctagtcac gagcaggcag cagctgcatt gaaaaatgct 300
ggccaggctg tcacaattgt tgcacaatat cgacctgaag aatacagtcg ttttgaagct 360
gcggccgcag gtgcgccggt gccgtatccg gatccgctgg aaccgcgtgc cgcatagact 420
gttgaaagtt gtttagcaaa acctcataca gaaaattcat ttactaacgt ctggaaagac 480
gacaa 485

<210> 11
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<213> Artificial Sequence

<220>
<223> HA peptide

<400> 11

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
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<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Tat protein

<400> 12

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 13
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> hCASK ligand

<400> 13

Gln Lys Ala Pro Thr Lys Glu Phe Tyr Ala
1 5 10

<210> 14
<211> 21
<212> DNA
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<220>
<223> pCAN5' primer

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21

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> pCAN3' primer

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20

<210> 16
<211> 59
<212> DNA
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 <222> (37)..(38)
 <223> n is a, c, g, or t

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 <223> m is a or c

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<220>
 <223> NNK2A

<400> 17
 aaaatgaatg aattgaatca ttg 23

<210> 18
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 <223> n is a, c, g, or t

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 <222> (35)..(36)

<223> n is a, c, g, or t

<220>

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<222> (22)..(25)

<223> m is a or c

<220>

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<222> (24)..(24)

<223> m is a or c

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<210> 19

<211> 21

<212> DNA

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<223> NNK3A

<400> 19

gaaatgcgtg gttctattac c 21

<210> 20

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<212> DNA

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<222> (185)..(186)

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<222> (191)..(192)

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<222> (335)..(336)

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<222> (344)..(345)

<223> n is a, c, g, or t

<220>

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<222> (347)..(348)
 <223> n is a, c, g, or t

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 <222> (193)..(193)
 <223> k is g or t

<220>
 <221> misc_feature
 <222> (337)..(337)
 <223> k is g or t

<220>
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 <222> (346)..(349)
 <223> k is g or t

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 tatggaaaat gttaccctg ttcgtttagt tcaatttcaa aaaaataccg atgaaccann 180
 kggtnnkacc nkkaaatga atgaattgaa tcattgtatt gttgcccgta ttatgcatgg 240
 tggatgatt catcgtcaag gtactttgca tgttggtgat gaaattcgtg aaattaatgg 300
 tatttctgtt gccaatcaaa ccggtgaaca attgnnkaaa atgnnknnkg aaatgcgtgg 360
 ttctattacc tttaaaattg ttccatctta tcgtacccaa tcttcttctg gaattcatgc 420
 ggccgcaggt gcgccggtgc cgtatccgga tccgctggaa ccgcgtgccg catagactgt 480
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<210> 21
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 <212> DNA
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 <223> b is c, g or t

<220>
 <221> misc_feature
 <222> (38)..(38)
 <223> k is g or t

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 <222> (26)..(26)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (31)..(31)

<223> r is a or g

<400> 21

caatgattca attcattcat ttttaanggta rbacccaktg gttcatcggt attttttttg 59

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<211> 23

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<223> TSM2A

<400> 22

aaaatgaatg aattgaatca ttg 23

<210> 23

<211> 59

<212> DNA

<213> Artificial Sequence

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<223> TSM2B

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<220>

<221> misc_feature

<222> (36)..(36)

<223> k is g or t

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<222> (22)..(25)

<223> m is a or c

<220>

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<222> (34)..(34)

<223> m is a or c

<220>

<221> misc_feature

<222> (35)..(35)

<223> w is a or t

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<222> (23)..(23)

<223> y is c or t

<400> 23

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<210> 24
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TSM3A

<400> 24
 gaaatgcgtg gttctattac c

21

<210> 25
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 <213> Artificial Sequence

<220>
 <223> hCASK PDZ

<220>
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 <223> k is g or t

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 <221> misc_feature
 <222> (346)..(349)
 <223> k is g or t

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 <222> (179)..(179)
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<220>
 <221> misc_feature
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 <223> m is a or c

<220>
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 <222> (344)..(344)
 <223> m is a or c

<220>
 <221> misc_feature
 <222> (191)..(191)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
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 <223> r is a or g

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 <222> (185)..(185)
 <223> v is a, c or g

<220>
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 <222> (336)..(336)

<223> w i s a o r t

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<221> misc_feature

<222> (186)..(186)

<223> y i s c o r t

<400> 25

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attcgcaatt ccttttagttg ttccttttcta tgcggccag cgggccggat ccggtatgga      120
tatggaaaat gttaccctgtg ttcgtttagt tcaatttcaa aaaaataccg atgaaccamt      180
gggtvytacc nttaaaatga atgaattgaa tcattgtatt gttgcccgtg ttatgcatgg      240
tggtatgatt catcgtcaag gtactttgca tgttggtgat gaaattcgtg aaattaatgg      300
tatttctggt gccaatcaaa ccgttgaaca attgmwkaaa atgmtkarkg aaatgcgtgg      360
ttctattacc tttaaaattg ttccatctta tcgtacccaa tcttcttctg gaattcatgc      420
ggccgcaggt gcgccggtgc cgtatccgga tccgctggaa ccgcgtgccg catagactgt      480
tgaaagttg                                     489
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<210> 26

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> C-terminus of BclA

<400> 26

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Ser Ala Ser Ile Ile Ile Glu Lys Val Ala
1           5           10
```

<210> 27

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide

<400> 27

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His Arg Arg Ser Ala Arg Tyr Leu Asp Thr Val Leu
1           5           10
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<210> 28

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide ligand of the third PDZ domain of human Dlg1

<400> 28

Ser Ser Leu Gln Ser Leu Glu Thr Ser Val
1 5 10